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BAD (SEQ ID NO:2) protein. The closed rectangle represents the BH3 domain of the longer murine BAD (SEQ ID NO:2) protein. "S112," S136" and "S155" indicate the location of serine residues at positions 112, 136 and 155 of the longer murine BAD (SEQ ID NO:2) protein, respectively. The amino acid sequences are those of BAD (SEQ ID NO:4), BAK (SEQ ID NO:5), BAX (SEQ ID NO:6), BIK (SEQ ID NO:7), BID (SEQ ID NO:8), HRK (SEQ ID NO:9), BOK (SEQ ID NO:10), and BIM (SEQ ID NO:11). Residues surrounded by a black box are identical. Residues surrounded by a gray box are homologous among BH3 domains. The code for the individual residues is A = alanine, C = cysteine, D = aspartic acid, E = glutamic acid, F = phenylalanine, G

Please replace the paragraph encompassing lines 4-11, page 32, with the following paragraph:

A2
Fig. 3(B) is a graphical representation of the results of an *in vitro* competition binding assay. Recombinant GST-Bcl-X_L was incubated with a BAD BH3 peptide (residues 143-168 of SEQ ID NO: 2) phosphorylated on Ser155 ("BAD BH3-P"), a BAD BH3 peptide (residues 143-168 of SEQ ID NO: 2) unphosphorylated on Ser155 ("BAD BH3"), or a BAK BH3 peptide (residues 71-89; residues 1-20 of SEQ ID NO: 5) as a positive control, at the indicated concentrations. The reaction mixtures were then added to microtiter plates pre-coated with BAK BH3 peptide. The amount of bound GST-Bcl-X_L was determined by ELISA using an anti-GST primary antibody and a horse-radish peroxidase-conjugated anti-mouse IgG secondary antibody with ABTS as substrate.
